

0987334-06004  
T09090" T25/850

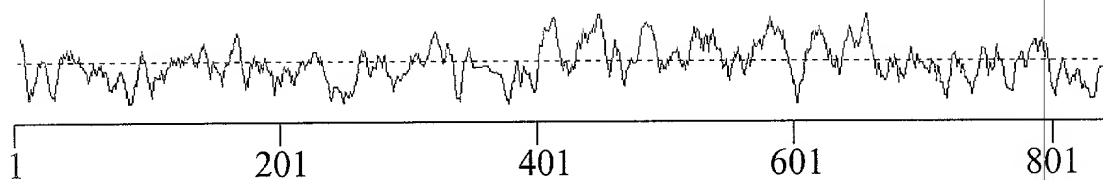


Figure 1

ion\_trans: domain 1 of 1, from 472 to 661: score 0.1, E = 1.2  
 (SEQ ID NO:9) \*->ilfildllfvllfllleivlkfiayglkstsniaakylksifnildll  
 ++ i + ++f++ ++l +++ ++ y +++ +  
 52906 472 DWRIAMTYERIFFICLEILVCAIHPI-----PGNYTFTWTA-RLAF 511  
 ailpllllllvflslgteqvakkrlrerfslelsqwyrylrlrllR  
 ++ p+ + + + l++ +Lrl+  
 52906 512 SYAPS--TTTADVDI-----LSIPMFLRLYL 536  
 lLrllrllrrletlf.e.....fe.lgtlawslqslgralksilrfllll  
 + r++ ++ +lf+ ++++++ l ++ +k+++ ++ +  
 52906 537 ---IARVMLLHSKLFtDtssrsIGaLNKI--NFNTRFVMKTLMTICPGT 580  
 lllligfsvigyllfkgyedlsenevdgnsefssyfdafyflfvltttvG  
 +ll++ s+ ++++ + + +e+ d+ + s++ a++ +t++++G  
 52906 581 VLLVF--SISLWIIAAWTVRACERYHDQQDVTSNFLGAMWLISITFLSIG 628  
 fGdlvpvwlgiiffvlfffiivgllllnlliavi<-\*  
 +Gd+vp++++ ++l+ i+g ++l +av+  
 52906 629 YGDMVPNTYCGKGVCLLTGIMGAGCTALVVAVV 661

Figure 2

09875321-060601

09875321.060601

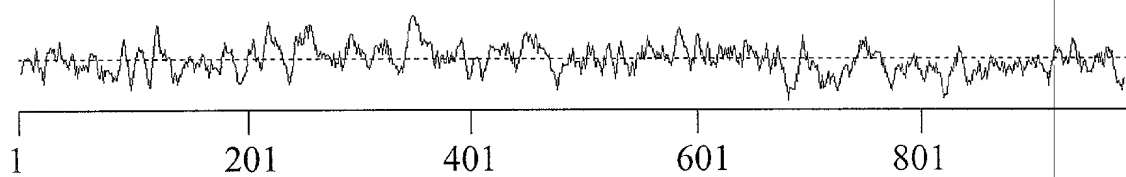


Figure 3

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ion_trans: domain 1 of 1, from 247 to 467: score 94.8, E = 1.7e-24
  (SEQ ID NO:9) *->ilfildllfvllflleivlkfiayglkstsn.....iaak
    +l ld + +++fl++ivl+f+ + + +++++ +++++ i++
33408      247      WLV-LDSVVDVIFLVDIVLNFH-TT----FVgpggevisdpklIRMN 287

    ylkSifnildllailplllllvflslgteqvakkrlrerfslelsqwyyr
    ylk++f +dll++lp++++ ++ +++
33408      288      YLKTWfV-IDLLSCLPYDIINAFENVDE-----G 315

    ilrflrlLrllRlLrllrllrrletlfefelgtlaWslqslg.ralksil
    i +++++L+ +R llrl r+ ++ l + l +++ ++
33408      316      ISSLFSSSLKVVR---LLRLGRVARK-----LDHY---LEYGAaVLVLLVC 354

    rfllllllllligfsvigyllfkgyedlse.....
    f+l++++l +++++ ig + + ++ + +++ + +++ ++
33408      355      VFGLVAHWLACIWYSIGDYEVIDEVTNTIqidswlyqlalsigtpyrynt 404

    ...nevdgnsefssyfdafyflfvltttvGfGdlvpv.wlgiiffvlfifi
    + + +++g+s+ s y ++yf++++l+t+GfG++ p++ +++f v++++
33408      405      sagIWEggPSKDSLIVSSLYFTMTSLTTIGFGNIAPTtDVEKMFSVAMMM 454

    ivgl111nlliavi<-*
    +++ ll ++++++
33408      455      VGS-LLYATIFGNV 467

```

Figure 4A

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cNMP_binding: domain 1 of 1, from 565 to 655: score 78.3, E = 1.5e-19
  (SEQ ID NO:10) *->aleersypaGeviirqGdpGdsfYivlsGeveykltedGartpevs
    ++ + ++G+ i++ G+ d + +v+sG++ev++
33408      565      EFQTIHCAPGDLIYHAGESVDALCFVVSGSLEVIQ----- 599

    qkqdtreqvvatlGpGdfFGElalltndgnknavlpsldqgaprtatvra
    +++vva+lg+Gd+FG++ + + + +a+ a+vra
33408      600      -----DDEVVAILGKGDVFGDIFW-KE-----TTLAHACANVRA 632

    ltdsellrldredFrrllqkype<-*
    lt+++l+ + re+++ +l+ y +
33408      633      LTYCDLHIIKREALLKVLDfYTA 655

```

Figure 4B

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33408  
rat EAG2  
(SEQ ID NO:12)

MPGGKRGLVA PQNTFLENIV RRSSESSFLG GNAQIVDWPV VYSNDGFCKL  
MPGGKRGLVA PQNTFLENIV RRSSESSFLG GNAQIVDWPV VYSNDGFCKL

SGYHRADV MQ KSSTCSFMYG ELTDKKTIEK VRQTFDNYES NCFEVLKYK  
SGYHRADV MQ KSSTCSFMYG ELTDKKTIEK VRQTFDNYES NCFEVLKYK

NRTPVWFY MQ IAPIRNEHEK VVLFLCTFKD ITLTKQPIED DSTKGWTKFA  
NRTPVWFY MQ IAPIRNEHEK VVLFLCTFKD ITLTKQPIED DSTKGWTKFA

RLTRALTNSR SVLQQLTPMN KTEVVHKHSR LAEVLQLGSD ILPQYKQEAP  
RLTRALTNSR SVLQQLTPMN KTETVHKHSR LAEVLQLGSD ILPQYKQEAP

KTPPHIILHY CAFKTTWDWV ILILTFYTAI MVPYNVSFKT KQNNIAWLVL  
KTPPHIILHY CAFKTTWDWV ILILTFYTAI MVPYNVSFKT KQNNIAWLVL

DSVVDVIFLV DIVLNFHTTF VGPGEVVISD PKLIRMNYLK TWFVIDLLSC  
DSVVDVIFLV DIVLNFHTTF VGPGEVVISD PKLIRMNYLK TWFVIDLLSC

LPYDIINAFE NVDEGISSLF SSLKVVRLLR LGRVARKLDH YLEYGA AVL  
LPYDIINAFE NVDEGISSLF SSLKVVRLLR LGRVARKLDH YLEYGA AVL

LLVCVFGLVA HWLACIWYSI GDYEVIDEVT NTIQIDSWLY QLALSIGTPY  
LLVCVFGLVA HWLACIWYSI GDYEVIDEVT NTIQIDSWLY QLALSIRTPY

RYNTSAGIWE GGPSKDSLYV SSlyFTMTSL TTIGFGNIAP TTDVEKMFSV  
RYNTSAGIWE GGPSKDSLYV SSlyFTMTSL TTIGFGNIAP TTDVEKMFSV

AMMMVGSLLY ATIFGNVTI FQMYANTNR YHEMLNNVRD FLKLYQVPKG  
AMMMVGSLLY ATIFGNVTI FQMYANTNR YHEMLNNVRD FLKLYQVPKG

LSERVMDYIV STWSMSKGID TEKVLSICPK DMRADICVHL NRKVFNEHPA  
LSERVMDYIV STWSMSKGID TEKVLSICPK DMRADICVHL NRKVFNEHPA

FRLASDGCLR ALAVEFQTIH CAPGDLIYHA GESVDALCFV VSGSLEVIQD  
FRLASDGCLR ALAVEFQTIH CAPGDLIYHA GESVDALCFV VSGSLEVIQD

DEVVAILGKG DVFGDIFWKE TTLAHACANV RALTYCDLHI IKREALLKVL  
EEVVAILGKG DVFGDIFWKE TTLAHACANV RALTYCDLHI IKREALLKVL

Figure 4C

DFYTAFANSF SRNLT LTCNL RKRIIFRKIS DVKKEEEEERL RQKNEVTL SI  
DFYTAFANSF SRNLT LTCNL RKRIIFRKIS DVKKEEEEERL RQKNEVTL SI

PVDHPVRKLF QKFKQQKELR NQGSTQGDPE RNQLQVESRS LQNGTSITGT  
PVDHPVRKLF QKFKQQKELR NQGSAQSDPE RSQLQVESRP LQNGASITGT

SVVTVSQITP IQTSLAYVKT SESLKQNNRD AMELKPNGGA DQKCLKVNSP  
SVVTVSQITP IQTSLAYVKT SETLKQNNRD AMELKPNGGA EPKCLKVNSP

IRMKNGNGKG WLRLKNNMGA HEEKKEDWNN VTKAESMGLL SEDPKSSDSE  
IRMKNGNGKG WLRLKNNMGA HEEKKEEWN VTKAESMGLL SEDPKGSDSE

NSVTKNPLRK TDSCDSGITK SDLRLDKAGE ARSPLEHSPI QADAKHPFYP  
NSVTKNPLRK TDSCDSGITK SDLRLDKAGE ARSPLEHSPS QADAKHPFYP

IPEQALQTTL QEVKHELKED IQLLS CRM TA LEKQVAEILK ILSEKSV PQA  
IPEQALQTTL QEVKHELKED IQLLS CRM TA LEKQVAEILK LLSEKSV PQT

SSPKSQMPLQ VPPQIPCQDI FSVSRPESPE SDKDEIHF  
SSPKPQIPLQ VPPQIPCQDI FSVSRPESPE SDKDEINF

Figure 4D

09875341.050604

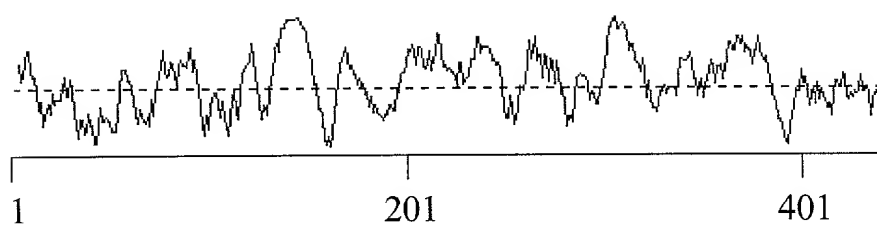


Figure 5

K\_tetra: domain 1 of 1, from 3 to 101: score 169.0, E = 7.9e-47  
 (SEQ ID NO:11) \*->ErvrLNVGGkrFeTskstLtrfkpdTlLgrllktdsdvhearlrld  
 Er++LNV G+rFeT+++TL rf pdTlLg++++ r ++  
 12189 3 ERLVLNVAGLRFETRARTLGRF-PDTLLGDPAR-----R-GR 37  
 fyddetgEyFFDRsPkhFetILnfYRtGdGkLhrp.evclidsfleEleFy  
 fydd++ EyFFDR++++F+++L++Y++G G+L+rp +v+ld+fleE +Fy  
 12189 38 FYDDARREYFFDRHRPSFDAVLYYYQSG-GRLRRPaHVPLDVFLEEVAFY 86  
 gldelaiesCcedey<-\*  
 gl+ a++ +ede+  
 12189 87 GLGAAALARLREDEG 101

Figure 6A

ion\_trans: domain 1 of 1, from 198 to 383: score 144.8, E = 1.5e-39  
 (SEQ ID NO:9) \*->ilfildllfvllflleivlkfiayglkstsniakylksifnildll  
 ++f++++l++ +f +e++++ ++ k a ++k+++n++d+  
 12189 198 PFFVETLCICWFSPELLVRLLCPSK-----AIFFKNVMLIDFV 238  
 ailplllllvflsgteqvakkrlrerfslelsqwyrrilrflrlLrllR  
 ailp+++ l+ l+++ +++++ +L +lR  
 12189 239 AILPYFVALGTELARQ-----RGVGQQAMSLAILR 268  
 lLrllrllrrletlfefelgtlaWslqslg.ralksilrflllllllllig  
 ++rl+r++r ++ + +++ lq+lg+++ +s+ ++ll+++l+ig  
 12189 269 VIRLVRFVRIFKLSR---HSGK---LQILGqTLRASMRELGLLIFFLFIG 312  
 fsvigyllfkgyedlsenevdgnsefssyfdafyflfvltttvGfGdlvp  
 + +++ +++++ + d+ +s f+s++++f++++vt+ttvG+Gd+ p  
 12189 313 VVLFSSAVYFAEVDRV-----DSHFTSIPESFWWAVVTMTTVGYGDMAP 356  
 v.wlgiiffvlfiiivgllllnlliavi<-\*  
 v+++g+i++ ++++i+g+l+++l+++vi  
 12189 357 VtVGGKIVG-SLCAIAGVLTISLPVPVI 383

Figure 6B

